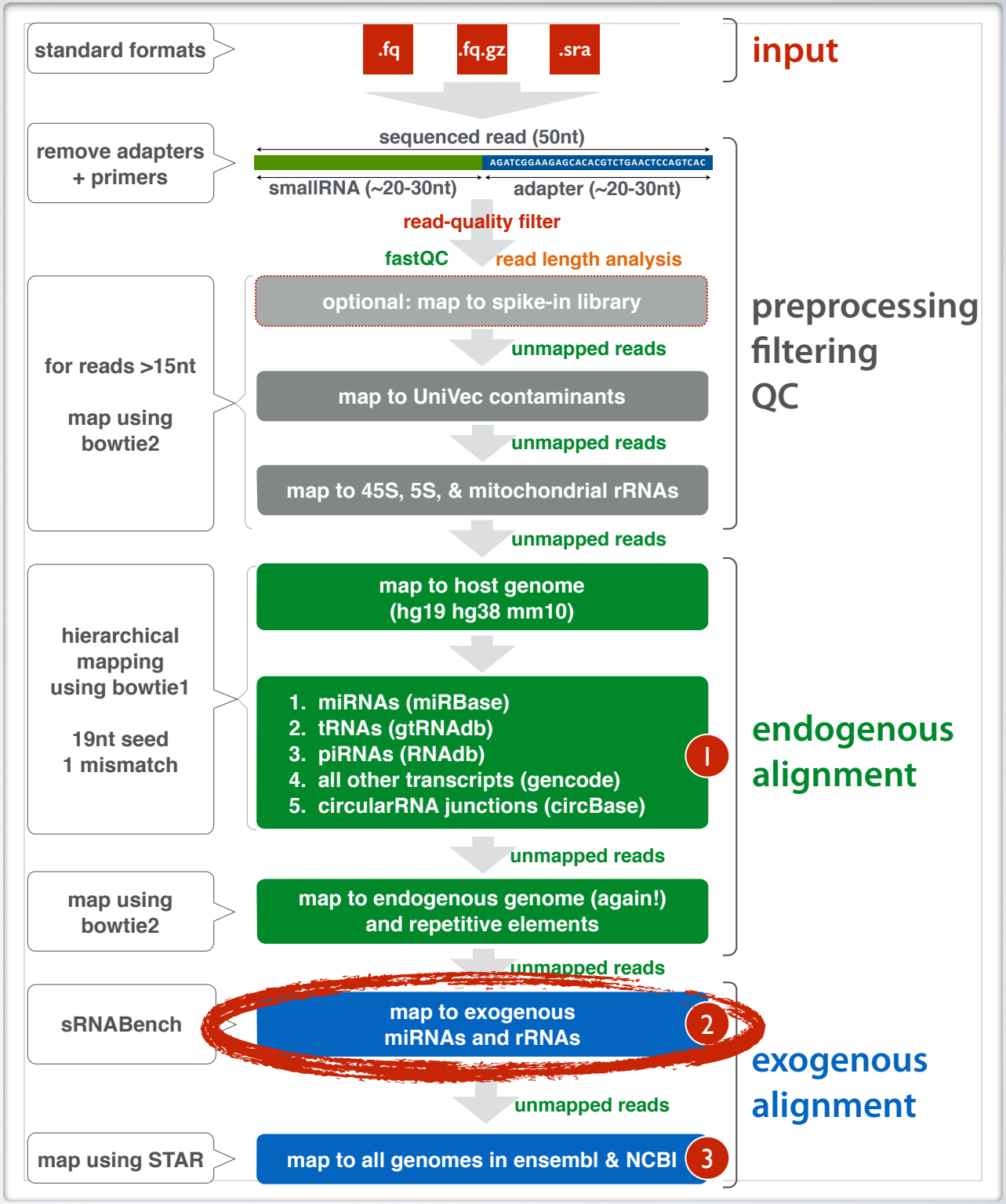
exceRpt

- **replaced sRNAbench** with custom alignments & quantification code

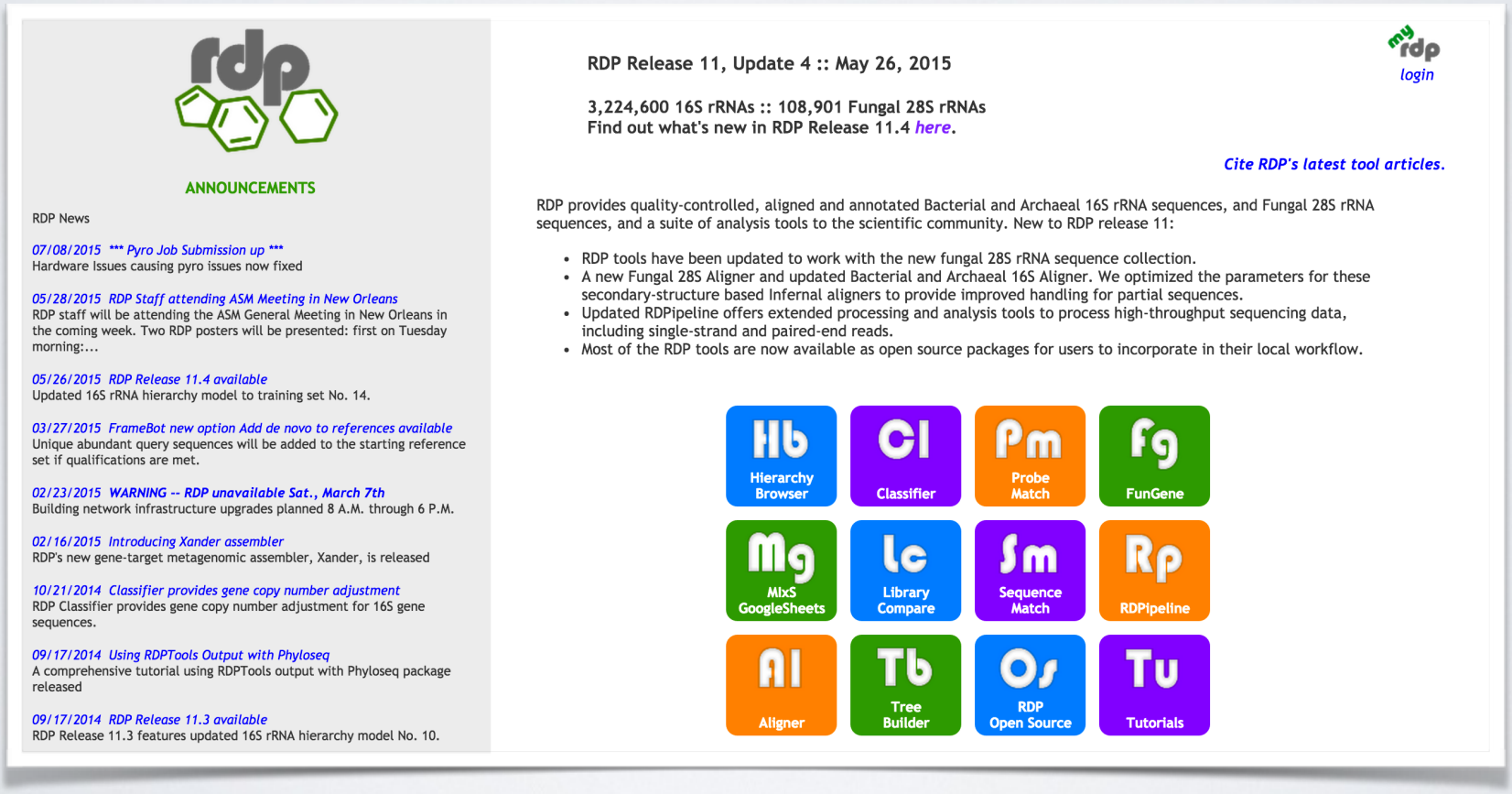
- **advantages**:
  - more alignment control
  - uses read qualities
  - support for 4N barcodes
  - faster
  - better memory usage
  - streamlined output files

- **alignment to rRNAs in RDP**
  - interpret/filter exogenous genome alignments
  - better compatibility with microbiome analyses



exogenous rRNA alignment

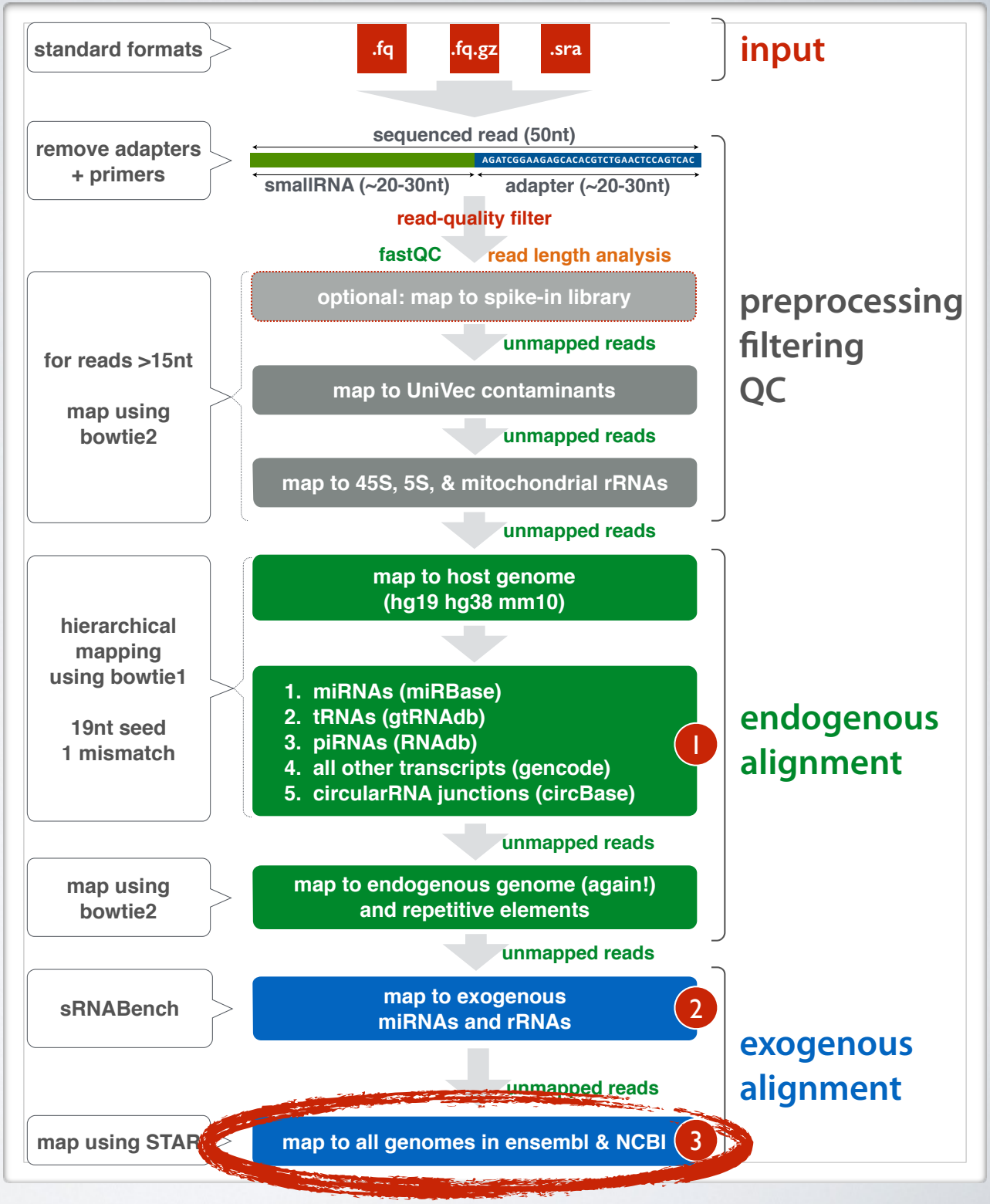
- can better compare exRNA results with microbiome results
- 16S and 28S sequences from the ribosome database:



exceRpt

- **replaced sRNAbench** with custom alignments & quantification code

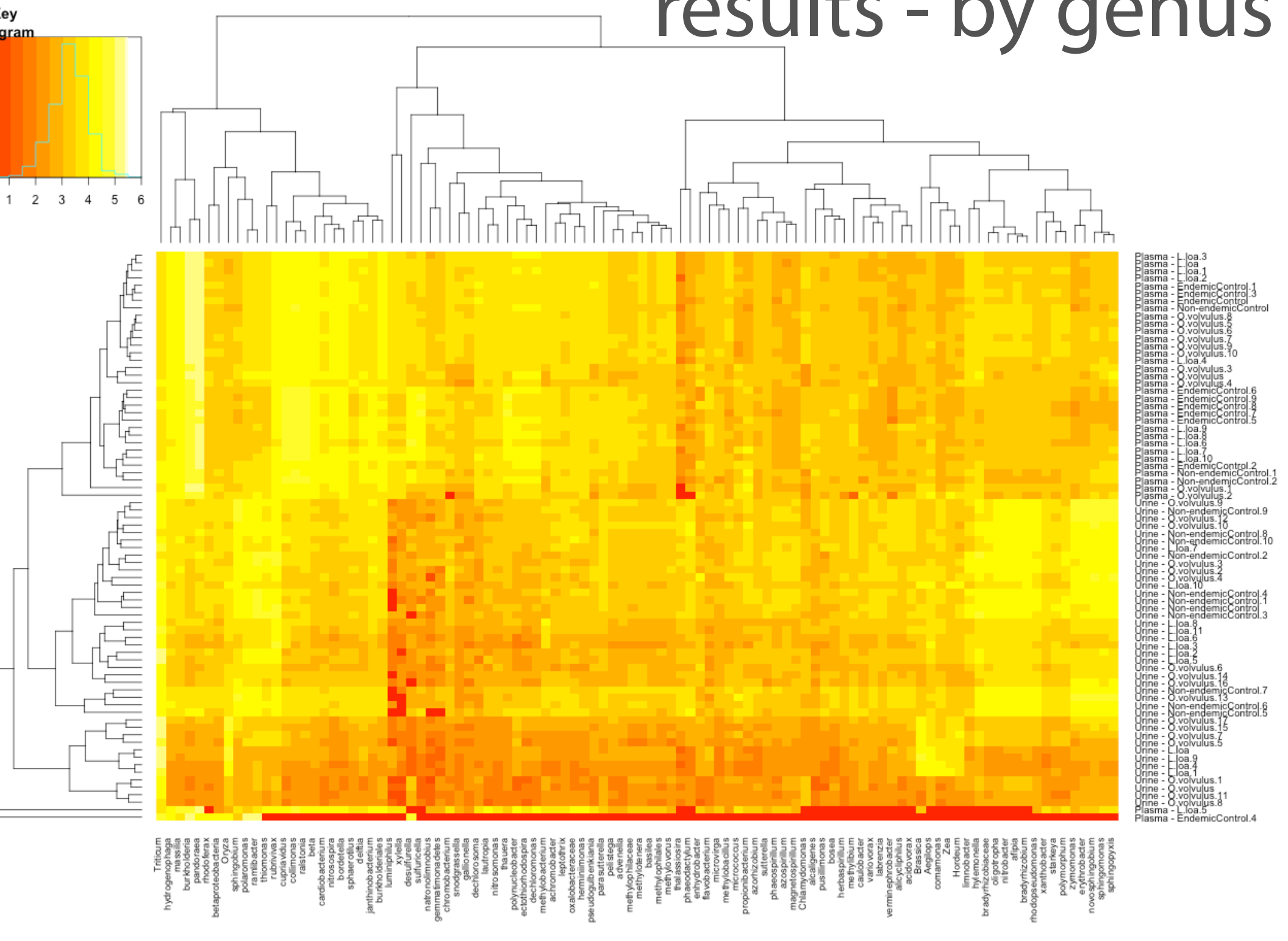
- **advantages**:
  - more alignment control
  - uses read qualities
  - support for 4N barcodes
  - faster
  - better memory usage
  - streamlined output files



exogenous genomes - new dataset

- collaboration with Amy Buck @ Edinburgh University
- 76 samples from Ghanaian individuals in a few groups:
  - healthy controls
  - infected by nematodes that cause onchocerciasis or "river blindness": 'Onchocerca volvulus' or 'Loa loa'
- samples from either plasma or urine

results - by genus



results - by genus